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OM protein - protein search, using SW model

Run on: October 18, 2005, 13:28:04 / Search time 166 Seconds
(without alignments)
62.907 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59
Perfect score: 27
Sequence: 1 FFAVANGNELLDLSLTVMNTEPERT 27

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20015:*\n5: geneseqp20028:*\n6: geneseqp20038a:*\n7: geneseqp2003bs:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	90	3	AA51476 Human TRF
2	27	100.0	90	3	AA28938 T cell re
3	27	100.0	90	3	AA87679 Feline hu
4	27	100.0	92	3	AA51475 Human TRF
5	27	100.0	92	3	AA28937 T cell re
6	27	100.0	92	3	AA87678 Feline hu
7	27	100.0	97	2	AA12123 TRFP chat
8	27	100.0	97	3	AA51472 Human TRF
9	27	100.0	97	3	AA28935 T cell re
10	27	100.0	97	3	AA90105 Cat TRFP
11	27	100.0	97	3	AA87675 Feline hu
12	27	100.0	100	8	AD038397 Cat aller
13	27	100.0	107	7	AD62496 Cat aller
14	27	100.0	109	2	AA12122 TRFP I ch
15	27	100.0	109	2	AA41985 Human T c
16	27	100.0	109	2	AA36541 TRFP chat
17	27	100.0	109	2	AA25593 Fells sp.
18	27	100.0	109	3	AA51471 Human TRF
19	27	100.0	109	3	AA28934 T cell re
20	27	100.0	109	3	AA90104 Cat TRFP
21	27	100.0	109	3	AA87674 Feline hu
22	27	100.0	109	7	AD03843 Cat aller
23	27	100.0	109	8	ADM12179 Cat aller
24	27	100.0	110	2	AA27370 TRFP chat
25	27	100.0	111	2	AA12121 TRFP chat

26	27	100.0	111	2	AA27369 Human TRF
27	27	100.0	111	3	AA51470 Human TRF
28	27	100.0	111	3	AA28933 T cell re
29	27	100.0	111	3	AA90103 Cat TRFP
30	27	100.0	111	3	AA87673 Feline hu
31	26	96.3	26	2	AA41977 Human T c
32	26	96.3	26	2	AA36544 Peptide Z
33	26	96.3	26	3	AA51481 Human TRF
34	26	96.3	26	3	AA28943 Peptide Z
35	26	96.3	26	3	AA90109 Cat TRFP
36	26	96.3	26	3	AA87684 Feline hu
37	26	96.3	96	2	AA36548 Recombito
38	26	96.3	96	3	AA28979 Peptide Y
39	26	96.3	96	3	AA90145 TRFP fusi
40	19	70.4	82	3	AA51478 Human TRF
41	19	70.4	82	3	AA28940 T cell re
42	19	70.4	82	3	AA90106 Cat TRFP
43	19	70.4	82	3	AA87681 Feline hu
44	19	70.4	101	2	AA27372 TRFP chat
45	18	66.7	18	3	AA51487 Human TRF

ALIGNMENTS

RESULT 1
AA51476
ID AA51476 standard; protein; 90 AA.

AA51476;

22-MAY-2000 (first entry)

Human TRFP chain 2 (short form) protein fragment #2.

T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
down regulation; immune response; allergen; immunoglobulin E;
sensitivity; cat protein allergen; human; chain 2.

Homo sapiens.

US6019972-A.

01-FEB-2000.

02-SEP-1994; 94US-00300928.

03-NOV-1989; 89US-00431565.

28-FEB-1991; 91US-00662276.

13-DEC-1991; 91US-00807529.

25-MAR-1992; 92US-00857311.

15-MAY-1992; 92US-00884718.

15-JAN-1993; 93US-00061116.

(IMMU-) IMMUNOLOGIC PHARM CORP.

Garman RD, Greenstein JL, Kuo M, Briner TU, Morville M;

Geffer ML;

WPI, 2000-146862/13.

Peptides of human T cell reactive feline protein for treating sensitivity

to cat protein allergens comprise at least one T cell epitope recognized

by a T cell receptor specific for the human T cell reactive feline

protein.

Example 1; Col 83-84; 105pp; English.

This invention describes a novel peptide (I) of human T cell reactive
feline protein (hTRFP) having at least one T cell epitope recognized by a
T cell receptor specific for the human T cell reactive feline protein,
the peptide consisting of at least 7-30 amino acids, and having an amino
acid sequence derived from an amino acid sequence comprising 94, 96, 97,

CC 109, or 111 residues, given in the specification. The peptides down
 CC regulate the immune response to the allergen. The peptides have reduced
 CC immunoglobulin E binding and reduce T cell responsiveness. The peptide
 CC (I) is useful in compositions for treating sensitivity to a cat protein
 CC allergen in a subject. This sequence represents the human TRFP chain 2
 CC (short form)

XX Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.9e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLDLSLTKNATEPERT 27
 DB 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 2

AA28938 standard; protein; 90 AA.

XX AAB28938;

DT 29-JAN-2001 (first entry)

DB T cell reactive feline protein chain 2 PRO short.

KW Cat; allergy; human T cell reactive feline protein; hTRFP; immunotherapy.

OS Felis sp.

PN US6120769-A.

PD 19-SEP-2000.

PF 28-APR-1995; 95US-00431184.

PR 03-NOV-1989; 89US-00431565.

PR 28-FEB-1991; 91US-00662276.

PR 13-DEC-1991; 91US-00807529.

PR 25-MAR-1992; 92US-00857311.

PR 15-MAY-1992; 92US-00884718.

PR 15-JAN-1993; 93US-00006116.

PR 02-SEP-1994; 94US-00300928.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Geffer ML, Garman RD, Greenstein JL, Bond JF;

PT WPI; 2000-601477/57.

XX Detecting, preventing and treating sensitivity to cat protein allergen

XX comprises combining a biological sample with a human T cell reactive

XX feline protein and determining the extent of binding that occurs.

XX Disclosure; Fig 7; 106pp; English.

XX The present invention relates to the detection of sensitivity to a cat

XX protein allergen by combining a blood sample from a subject with a

XX peptide of human T cell reactive feline protein (hTRFP). This method and

XX the hTRFP peptides are useful for diagnosing, preventing and treating cat

XX allergies by reducing or abolishing an individual's allergic response to

XX a cat allergen. DNA encoding the TRFP may be used as probes to locate

XX equivalent sequences present in other species. These may further be used

XX to study the mechanism of immunotherapy of cat allergy, and to design

XX modified derivatives, analogues or functional equivalents useful in

XX immunotherapy. The present sequence was used in the invention

XX Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.9e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLDLSLTKNATEPERT 27

DB 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 3

AA87679

AA87679 standard; protein; 90 AA.

XX AAV87679;

DT 22-AUG-2000 (first entry)

DB Feline human TRFP chain 2 short form protein #2.

KW T-cell reactive feline protein; TRFP; Fel d I; cat allergen;

OS antiallergic; T cell stimulator; diagnostic; immunotherapy.

PN Felis sp.

PD US6048962-A.

PF 11-APR-2000.

PR 27-APR-1995; 95US-00430014.

PR 03-NOV-1989; 89US-00431565.

PR 28-FEB-1991; 91US-00662276.

PR 13-DEC-1991; 91US-00807529.

PR 25-MAR-1992; 92US-00857311.

PR 15-MAY-1992; 92US-00884718.

PR 15-JAN-1993; 93US-00006116.

PR 02-SEP-1994; 94US-00300928.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Kuo M, Rogers BL, Geffer ML, Morgenstern JP, Brauer AW;

PT Greenstein JL, Griffith ID, Garman RD;

XX WPI; 2000-316905/27.

XX New human T cell reactive feline protein useful for reducing or

XX abolishing individual's allergic response to cat allergen comprising two

XX different covalently linked peptide chains.

XX Example 2; Col 83-84; 106pp; English.

XX This invention describes a novel naturally occurring cat protein allergen

XX (I), human T cell reactive feline protein (TRFP), comprising two

XX different covalently linked peptide chains with a molecular weight of 20

XX kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD

XX under reducing conditions. The products of the invention have

XX antiallergic activity and act as human T cell stimulators. TRFP is useful

XX for reducing or preventing the adverse effects of cat allergens on cat

XX allergic individuals and in ex vivo diagnostic tests to determine which

XX cat peptides cause sensitivity so as to selectively use them to desensitize a

XX cat sensitive individual. Purified TRFP is also useful for studying the

XX mechanism of immunotherapy of cat allergy and to design modified

XX derivatives, analogs or functional equivalents that are more useful in

XX immunotherapy against cat allergy. DNA sequences encoding TRFP are useful

XX as probes to locate equivalent sequences present in other species (goats,

XX sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or

XX therapeutics. Fully defined and characterized TRFP provides complete and

XX a very simple desensitization therapy. This sequence represents a human T

XX cell reactive feline protein (also known as Fel d I) chain 2, short form

XX which is described in the method of the invention

XX Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.9e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
 |||||
 DB 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 4
 AAY51475
 ID AAY51475 standard; protein; 92 AA.

XX
 AC AAY51475;

XX 22-MAY-2000 (first entry)

XX Human TRFP chain 2 (long form) protein fragment #2.

XX T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
 KW down regulation; immune response; allergen; immunoglobulin E;
 KW sensitivity; cat protein allergen; human; chain 2.

XX Homo sapiens.

XX US6019972-A.

XX 01-FEB-2000.

XX 02-SEP-1994; 94US-00300928.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX (IMMUNO-) IMMUNOLOGIC PHARM CORP.

XX Garman RD, Greenstein JL, Kuo M, Briner TU, Morville M;

XX Gelfer ML;

XX WPI; 2000-146862/13.

XX Peptides of human T cell reactive feline protein for treating sensitivity

XX to cat protein allergens comprise at least one T cell epitope recognized

XX by a T cell receptor specific for the human T cell reactive feline

XX protein.

XX Example 1; Col 83-84; 105pp; English.

XX This invention describes a novel peptide (1) of human T cell reactive

XX feline protein (hTRFP) having at least one T cell epitope recognized by a

XX T cell receptor specific for the human T cell reactive feline protein.

XX the peptide consisting of at least 7-30 amino acids, and having an amino

XX acid sequence derived from an amino acid sequence comprising 94, 96, 97,

XX 109, or 111 residues, given in the specification. The peptides down

XX regulate the immune response to the allergen. The peptides have reduced

XX immunoglobulin E binding and reduce T cell responsiveness. The peptide

XX (1) is useful in compositions for treating sensitivity to a cat protein

RESULT 5
 ID: AAB28937 standard; protein; 92 AA.

XX AAB28937;

XX 29-JAN-2001 (first entry)

XX T cell reactive feline protein chain 2 PRO long.

XX Cat; allergy; human T cell reactive feline protein; hTRFP; immunotherapy.

XX Felis sp.

XX US6120769-A.

XX 19-SEP-2000.

XX 28-APR-1995; 95US-00431184.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX 02-SEP-1994; 94US-00300928.

XX (IMMUNO-) IMMUNOLOGIC PHARM CORP.

XX Gelfer ML, Garman RD, Greenstein JL, Bond JF;

XX WPI; 2000-601477/57.

XX Detecting, preventing and treating sensitivity to cat protein allergen

XX comprises combining a biological sample with a human T cell reactive

XX feline protein and determining the extent of binding that occurs.

XX Disclosure; Fig 7; 106pp; English.

XX The present invention relates to the detection of sensitivity to a cat

XX protein allergen by combining a blood sample from a subject with a

XX peptide of human T cell reactive feline protein (hTRFP). This method and

XX the hTRFP peptides are useful for diagnosing, preventing and treating cat

XX allergies by reducing or abolishing an individual's allergic response to

XX a cat allergen. DNA encoding the TRFP may be used as probes to locate

XX CC equivalent sequences present in other species. These may further be used

XX to study the mechanism of immunotherapy of cat allergy, and to design

XX modified derivatives, analogues or functional equivalents useful in

XX immunotherapy. The present sequence was used in the invention

XX Sequence 92 AA;

XX Query Match 100.0%; Score 27; DB 3; Length 92;

XX Best Local Similarity 100.0%; Pred. No. 3e-19;

XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
 |||||
 DB 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 6
 AAY87678
 ID AAY87678 standard; protein; 92 AA.

XX AAY87678;

XX 22-AUG-2000 (first entry)

XX Human TRFP chain 2 long form protein #2.

XX T-cell reactive feline protein; TRFP; fel d 1; cat allergen;

XX

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KM antiAllergic; T cell stimulator; diagnostic; immunotherapy.
XX
OS Felis sp.
XX
PN US6048962-A.
XX
PD 11-APR-2000.
XX
PF 27-APR-1995; 95US-00430014.
XX
PR 03-NOV-1989; 89US-00431565.
PR 28-FEB-1991; 91US-00662276.
PR 13-DEC-1991; 91US-00807529.
PR 25-MAR-1992; 92US-00857311.
PR 15-MAY-1992; 92US-00884718.
PR 15-JAN-1993; 93US-00006116.
PR 02-SEP-1994; 94US-00300928.
XX
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
PI Kuo M, Rogers BL, Gelfer ML, Morgenstern JP, Brauer AM,
PI Greenstein JL, Griffith ID, Garman RD;
XX
DR WPI; 2000-316905/27.
XX
PT New human T cell reactive feline protein useful for reducing or
PT abolishing individual's allergic response to cat allergen comprising two
PT different covalently linked peptide chains.
XX
PS Example 2; Col 81-84; 106pp; English.
XX
CC This invention describes a novel naturally occurring cat protein allergen
CC (I), human T cell reactive feline protein (TRFP), comprising two
CC different covalently linked peptide chains with a molecular weight of 20
CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
CC under reducing conditions. The products of the invention have
CC anti-allergic activity and act as human T cell stimulators. TRFP is useful
CC for reducing or preventing the adverse effects of cat allergens on cat
CC allergic individuals and in ex vivo diagnostic tests to determine which
CC peptides cause sensitivity so as to selectively use them to desensitize a
CC cat sensitive individual. Purified TRFP is also useful for studying the
CC mechanism of immunotherapy of cat allergy and to design modified
CC derivatives, analogs or functional equivalents that are more useful in
CC immunotherapy against cat allergy. DNA sequences encoding TRFP are useful
CC as probes to locate equivalent sequences present in other species (goats,
CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
CC therapeutics. Fully defined and characterized TRFP provides complete and
CC a very simple desensitization therapy. This sequence represents a human T
CC cell reactive feline protein (also known as Fel d I) chain 2, long form
CC which is described in the method of the invention
XX
SQ Sequence 92 AA;
XX
Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFAVANGNELLDLSLTKVNATEPERT 27
DB 14 FFAVANGNELLDLSLTKVNATEPERT 40
XX
RESULT 7
AAR12123
ID AAR12123 standard; protein; 97 AA.
XX
AC AAR12123;
XX
DT 26-JUL-1991 (first entry)
XX
DB TRFP chain 2 - truncated short form.
XX
KW Human T cell reactive feline protein; cat allergen.

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XX
OS Felis catus.
XX
FH Key Location/Qualifiers
FT Peptide 3..19
FT Protein /label= leader sequence
FT /label= TRFP I truncated short form
XX
PN WO9106571-A.
XX
PD 16-MAY-1991.
XX
PR 03-NOV-1989; 89US-00431565.
PR 03-NOV-1989; 89US-00431565.
XX
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
PI Gelfer ML, Garman RD, Greenstein JL, Juo M, Rogers BL, Brauer AM;
PI N-PSDB; AAQ11840.
XX
DR WPI; 1991-164136/22.
XX
PT New pure covalently linked human T cell reactive feline protein - and
PT modified peptide(s), used to reduce effects of cat allergens and to
PT diagnose sensitivity to allergens.
XX
PS Claim 2; Fig 5; 70pp; English.
XX
CC Poly-A mRNA from cat parotid and mandibular glands was used to produce
CC cDNA clones for both chain 1 and chain 2 of TRFP. These clones were then
CC used to screen a cat genomic library. Chain 1 exists in two forms having
CC different leader sequences (A and B). The sequence can be used to express
CC the protein and peptide deriva. which stimulate T-cells in persons
CC allergic to cats. The peptides can be used to reduce/eliminate the
CC allergic response partic. by modifcn. of lymphokine prodn. by the T-
CC cells. They can also be used to identify epitopes responsible for
CC sensitivity. The DNA can be used to detect comparable sequence in other
CC species, and also for prodn. of modified forms of TRFP esp. showing
CC reduced binding to IgE and thus reduced tendency to cause adverse
CC reactions. See also AAR12119-R12122
XX
SQ Sequence 97 AA;
XX
Query Match 100.0%; Score 27; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFAVANGNELLDLSLTKVNATEPERT 27
DB 33 FFAVANGNELLDLSLTKVNATEPERT 59
XX
RESULT 8
AAY51472
ID AAY51472 standard; protein; 97 AA.
XX
AC AAY51472;
XX
DT 22-MAY-2000 (first entry)
XX
DB Human TRFP chain 2 (truncated form) protein fragment.
XX
KW T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
KW down regulation; immune response; allergen; immunoglobulin E;
KW sensitivity; cat protein allergen; human; chain 2.
XX
OS Homo sapiens.
XX
PN US6019972-A.
XX
PD 01-FEB-2000.

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XX PF 02-SEP-1994; 94US-00300928.
XX PR 03-NOV-1989; 89US-00431565.
XX PR 28-FEB-1991; 91US-00662276.
XX PR 13-DEC-1991; 91US-00807529.
XX PR 25-MAR-1992; 92US-00857311.
XX PR 15-MAY-1992; 92US-00884718.
XX PR 15-JAN-1993; 93US-00006116.
XX PA (IMMU-) IMMUNOLOGIC PHARM CORP.
XX PI Garman RD, Greenstein JL, Kuo W, Briner TV, Morville M;
XX PI Gelfer ML;
XX DR WPI; 2000-146862/13.
XX DR N-PSDB; AA288619.
XX PT Peptides of human T cell reactive feline protein for treating sensitivity
XX PT to cat protein allergens comprise at least one T cell epitope recognized
XX PT by a T cell receptor specific for the human T cell reactive feline
XX PT protein.
XX PS Claim 1; Col 81-82; 105pp; English.
XX CC This invention describes a novel peptide (1) of human T cell reactive
XX CC feline protein (hTRP) having at least one T cell epitope recognized by a
XX CC T cell receptor specific for the human T cell reactive feline protein,
XX CC the peptide consisting of at least 7-30 amino acids, and having an amino
XX CC acid sequence derived from an amino acid sequence comprising 94, 96, 97,
XX CC 109, or 111 residues, given in the specification. The peptides down
XX CC regulate the immune response to the allergen. The peptides have reduced
XX CC immunoglobulin E binding and reduce T cell responsiveness. The peptide
XX CC (1) is useful in compositions for treating sensitivity to a cat protein
XX CC allergen in a subject. This sequence represents the human TRFP chain 2
XX CC (truncated form)
XX SQ Sequence 97 AA;

Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFAVANGNELLDLSTKVNATEPERT 27
DB 33 PFAVANGNELLDLSTKVNATEPERT 59

RESULT 9
AAB28935
ID AAB28935 standard; protein; 97 AA.
XX AC AAB28935;
XX DT 29-JAN-2001 (first entry)
XX DE T cell reactive feline protein chain 2 truncated form.
XX KW Cat; allergy; human T cell reactive feline protein; hTRP; immunotherapy.
XX OS Felis sp.
XX PN US6120769-A.
XX PD 19-SEP-2000.
XX PF 28-APR-1995; 95US-00431184.
XX PR 03-NOV-1989; 89US-00431565.
XX PR 28-FEB-1991; 91US-00662276.
XX PR 13-DEC-1991; 91US-00807529.
XX PR 25-MAR-1992; 92US-00857311.
XX PR 15-MAY-1992; 92US-00884718.

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PR 15-JAN-1993; 93US-00006116.
PR 02-SEP-1994; 94US-00300928.
XX PA (IMMU-) IMMUNOLOGIC PHARM CORP.
XX PI Garman RD, Greenstein JL, Bond JF;
XX PI Gelfer ML;
XX DR WPI; 2000-601477/57.
XX DR N-PSDB; AAC60105.
XX PT Detecting, preventing and treating sensitivity to cat protein allergen
XX PT comprises combining a biological sample with a human T cell reactive
XX PT feline protein and determining the extent of binding that occurs.
XX PS Claim 1; Fig 5; 106pp; English.
XX CC The present invention relates to the detection of sensitivity to a cat
XX CC protein allergen by combining a blood sample from a subject with a
XX CC peptide of human T cell reactive feline protein (hTRP). This method and
XX CC the hTRP peptides are useful for diagnosing, preventing and treating cat
XX CC allergies by reducing or abolishing an individual's allergic response to
XX CC a cat allergen. DNA encoding the TRFP may be used as probes to locate
XX CC equivalent sequences present in other species. These may further be used
XX CC to study the mechanism of immunotherapy of cat allergy, and to design
XX CC modified derivatives, analogues or functional equivalents useful in
XX CC immunotherapy. The present sequence was used in the invention
XX SQ Sequence 97 AA;

Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PFAVANGNELLDLSTKVNATEPERT 27
DB 33 PFAVANGNELLDLSTKVNATEPERT 59

RESULT 10
AAV90105
ID AAV90105 standard; protein; 97 AA.
XX AC AAV90105;
XX DT 12-SEP-2003 (revised)
XX DT 13-JUL-2000 (first entry)
XX DE Cat TRFP chain 2 truncated form protein sequence.
XX KW Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;
XX KW house dust; Fel d 1; cat allergy; Felis domesticus sensitivity; therapy;
XX KW diagnosis; goat; sheep; horse; rabbit; dog.
XX OS Felis catub.
XX PH Key Location/Qualifiers
XX FT Peptide 1..19 /note= "signal peptide"
XX FT Protein 20..97 /note= "mature TRFP chain 2 truncated form"
XX PN US6025162-A.
XX PD 15-FEB-2000.
XX PF 28-APR-1995; 95US-00430944.
XX PR 03-NOV-1989; 89US-00431565.
XX PR 28-FEB-1991; 91US-00662276.
XX PR 13-DEC-1991; 91US-00807529.
XX PR 25-MAR-1992; 92US-00857311.
XX PR 15-MAY-1992; 92US-00884718.
XX PR 15-JAN-1993; 93US-00006116.

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PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Morgenstern JP, Griffith IJ, Rogers BL;
 XX WPI, 2000-181812/16.
 DR N-PSDB; AAA07439.
 XX
 PT New human T cell reactive feline protein, useful for desensitizing cat
 XX allergic individuals to cat allergens.
 PS Claim 1; Fig 5; 108pp; English.
 XX
 CC This sequence is a peptide chain of the human T cell reactive feline
 CC protein (TRFP) of the invention. The protein is a cat protein allergen,
 CC and was isolated from a vacuum bag extract obtained by affinity
 CC purification of house dust collected from several homes with cats. TRFP
 CC is composed of two covalently linked peptide chains, and is also referred
 CC to as Fel d 1. TRFP and its peptides are useful for reducing or
 CC preventing the adverse effects that exposure to cat allergens normally
 CC has on cat allergic individuals (i.e. to desensitize individuals to cat
 CC allergens or block the effect of the allergens). TRFP is also used in
 CC methods of diagnosing sensitivity to feline domesticus in an individual.
 CC DNA sequences encoding TRFP can be used as probes to locate equivalent
 CC sequences present in other species, e.g. goat, sheep, horse, rabbit and
 CC dog, that may be useful in a diagnostic and/or therapeutic applications.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 97 AA;
 XX
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PFAVANGNELLDLSTKYNATEPERT 27
 DB 33 PFAVANGNELLDLSTKYNATEPERT 59
 XX
 RESULT 11
 AA87675
 ID AAY87675 standard; protein; 97 AA.
 XX
 AC AAY87675;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Feline human TRFP chain 2 truncated form protein.
 XX
 KW T-cell reactive feline protein; TRFP; Fel d 1; cat allergen;
 KW anti-allergic; T cell stimulator; diagnostic; immunotherapy.
 XX
 OS Feline sp.
 XX
 PN US6048962-A.
 XX
 PD 11-APR-2000.
 XX
 PF 27-APR-1995; 95US-00430014.
 XX
 PR 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00061116.
 PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Kuo M, Rogers BL, Gefter ML, Morgenstern JP, Brauer AW,
 PI Greenstein JL, Griffith IJ, Garman RD;

XX
 DR WPI, 2000-316905/27.
 DR N-PSDB; AAA12246.
 XX
 PT New human T cell reactive feline protein useful for reducing or
 PT abolishing individual's allergic response to cat allergen comprising two
 PT different covalently linked peptide chains.
 XX
 PS Claim 2; Col 79-80; 106pp; English.
 XX
 CC This invention describes a novel naturally occurring cat protein allergen
 CC (1), human T cell reactive feline protein (TRFP), comprising two
 CC different covalently linked peptide chains with a molecular weight of 20
 CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
 CC under reducing conditions. The products of the invention have
 CC anti-allergic activity and act as human T cell stimulators. TRFP is useful
 CC for reducing or preventing the adverse effects of cat allergens on cat
 CC allergic individuals and in ex vivo diagnostic tests to determine which
 CC peptides cause sensitivity so as to selectively use them to desensitize a
 CC cat sensitive individual. Purified TRFP is also useful for studying the
 CC mechanism of immunotherapy of cat allergy and to design modified
 CC derivatives, analogs or functional equivalents that are more useful in
 CC immunotherapy against cat allergy. DNA sequences encoding TRFP are useful
 CC as probes to locate equivalent sequences present in other species (goats,
 CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
 CC therapeutics. Fully defined and characterized TRFP provides complete and
 CC a very simple desensitization therapy. This sequence represents a human T
 CC cell reactive feline protein (also known as Fel d 1) chain 2, truncated
 CC form which is described in the method of the invention
 XX
 SQ Sequence 97 AA;
 XX
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PFAVANGNELLDLSTKYNATEPERT 27
 DB 33 PFAVANGNELLDLSTKYNATEPERT 59
 XX
 RESULT 12
 ADO38397
 ID ADO38397 standard; peptide; 100 AA.
 XX
 AC ADO38397;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Cat allergen Fel d1 MHC class II-presented epitope #5.
 XX
 KW Antibacterial; Virucide; Antiparasitic; Antiarthritic;
 KW Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;
 KW Immunosuppressive; Antidiabetic; Antithyroid; Antiasbatic;
 KW Antiallergic; Cytostatic; Antipneumatic; Gene Therapy; Vaccine;
 KW MHC Class II; II-key motif; Immune response; anthrax; EBOLA; HIV;
 KW influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;
 KW rickettsia; rheumatoid arthritis; multiple sclerosis;
 KW autoimmune thyroiditis; diabetes mellitus; myasthenia gravis;
 KW lupus erythematosus; scleroderma; dermatomyositis; pemphigus; asthma;
 KW allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;
 KW adenoma; cat; cat dander; fel d1.
 XX
 OS Feline catu.
 XX
 PN US2004058861-A1.
 XX
 PD 25-MAR-2004.
 XX
 PF 24-SEP-2002; 2002US-00253286.
 XX
 PR 24-SEP-2002; 2002US-00253286.
 XX
 PI

KW		Human T cell reactive feline protein; cat allergens.	
XX			
OS	Felis catus.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	3..19	/label= Leader sequence
FT	Protein	20..111	/label= TRFP I short form
XX			
PM	WO9106571-A.		
PD	16-MAY-1991.		
XX			
PF	03-NOV-1989;	89US-00431565.	
XX			
PR	03-NOV-1989;	89US-00431565.	
XX	(IMMU-) IMMUNOLOGIC PHARM COR.		
PA	Gelfer ML, Garman RD, Greenstein JL, Juo M, Rogers BL, Brauer AM;		
PI	MPJ, 1991-164136/22.		
DR	N-BSD; AAQ11839.		
PT	New pure covalently linked human T cell reactive feline protein - and modified peptide(s), used to reduce effects of cat allergens and to diagnose sensitivity to allergens.		
PS	Claim 2; Fig 4; 70pp; English.		
XX			
Poly-A mRNA from cat parotid and mandibular glands was used to produce			
CC	cDNA clones for both chain 1 and chain 2 of TRFP. These clones were then		
CC	used to screen a cat genomic library. Chain 1 exists in two forms having		
CC	different leader sequences (A and B). The sequence can be used to express		
CC	the protein and peptide derivs. which stimulate T-cells in persons		
CC	allergic to cats. The peptides can be used to reduce/eliminate the		
CC	allergic response partic. by modifcn. of lymphokine prodn. by the T-		
CC	cells. They can also be used to identify epitopes responsible for		
CC	sensitivity. The DNA can be used to detect comparable sequence in other		
CC	species, and also for prodn. of modified forms of TRFP esp. showing		
CC	reduced binding to IgE and thus reduced tendency to cause adverse		
CC	reactions. See also AAR12119-R12123		
SQ	Sequence 109 AA;		
Query Match	100.0%; Score 27; DB 2; Length 109;		
Best Local Similarity	100.0%; Pred. No. 3.5e-19;		
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
OY	1 PFAVANGNELLDLSITKNATEPERT 27		
DB	33 PFAVANGNELLDLSITKNATEPERT 59		
RESULT 15			
AAR41985			
ID	AAR41985 standard; protein; 109 AA.		
AC	AAR41985;		
XX			
DT	25-MAR-2003 (revised)		
DT	21-APR-1994 (first entry)		
DE	Human T cell reactive feline protein chain 2.		
XX			
KW	Human, T cell; reactive; feline; protein; immune response; antigen;		
KW	tolerance; mammal; Dermatophagoides; Felis; Ambrosia; Lolium; Canis;		
KW	Cryptomeria; Alternaria; Alder; Betula; Quercus; Olea; Artemisia;		
KW	Plantago; Parietaria; Blatella; Apis; Periplaneta; autoantigen.		
XX			
OS	Homo sapiens.		
XX			

```

FH Key Location/Qualifiers
FT Peptide 1..17
FT /note= "Signal peptide"
FT Protein 18..109
FT /note= "Mature protein"
XX
XX WO9319178-A2.
XX
XX 30-SEP-1993.
XX
XX 25-MAR-1993; 93WO-US002462.
XX
XX 25-MAR-1992; 92US-00857311.
XX 15-MAY-1992; 92US-00884718.
XX 15-JAN-1993; 93US-00006116.
XX
XX (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
XX Gelfer ML, Garman RD, Greenstein JL, Kuo M, Briner TV,
XX Morville M;
XX
XX WPI; 1993-320744/40.
XX
XX N-PSDB; AAQ49535.
XX
XX
XX New peptide(s) for inducing tolerance - comprise one or more epitope(s)
XX of an allergen administered subcutaneously, for treating sensitivity to
XX cats, bees, etc.
XX
XX
XX Disclosure; Fig 2; 107pp; English.
XX
XX
XX This sequence represents chain 2 of human T cell reactive feline protein
XX (TRFP). Peptides derived from TRFP may be used in a therapeutic
XX composition which is useful in treating diseases which involve an immune
XX response to a protein antigen. This composition may be used to induce
XX tolerance in a mammal to dermatophagides, Felis, Ambrosia, Lolium,
XX Cryptococcus, Alternaria, Alder, Betula, Quercus, Olea, Artemesia,
XX Plantago, Parietaria, Canis, Blatella, Apis, Periplaneta and to
XX autoantigens in humans. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 109 AA;
XX
XX Query Match 100.0%; Score 27; DB 2; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-19;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX 1 FFAVANGNELLDLSTKVNATEPERT 27
XX |||||||||||||||||||||
XX Db 31 FFAVANGNELLDLSTKVNATEPERT 57

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Search completed: October 18, 2005, 13:44:17
Job time : 167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:47:36 ; Search time 170 seconds

(without alignments)
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Perfect score: 27
Sequence: 1 FFAVANGNELLDLSLTKVNTBEPRT 27

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1860064 seqs, 416830855 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09C_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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- 19: /cgn2_6/ptodata/2/pubppaa/US11_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	107	14	US-10-295-903-4
2	27	100.0	109	8	US-08-464-363-6
3	27	100.0	109	10	US-09-847-208-98
4	27	100.0	109	15	US-10-245-871-136
5	27	100.0	109	15	US-10-463-113-6
6	27	100.0	109	15	US-10-253-286-136
7	27	100.0	109	16	US-10-809-689-32
8	26	96.3	26	8	US-08-464-363-9
9	26	96.3	26	15	US-10-463-113-9
10	26	96.3	96	8	US-08-464-363-39
11	26	96.3	96	15	US-10-463-113-39

12	16	59.3	21	8	US-08-464-363-17	Sequence 17, Appl
13	16	59.3	21	15	US-10-463-113-17	Sequence 17, Appl
14	15	55.6	15	8	US-08-464-363-19	Sequence 19, Appl
15	15	55.6	15	15	US-10-463-113-19	Sequence 19, Appl
16	14	51.9	92	16	US-10-809-689-5	Sequence 5, Appl
17	12	44.4	16	15	US-10-245-871-183	Sequence 183, App
18	12	44.4	16	15	US-10-253-286-183	Sequence 183, App
19	12	44.4	16	16	US-10-809-689-13	Sequence 13, Appl
20	12	44.4	21	15	US-10-245-871-188	Sequence 188, App
21	12	44.4	21	15	US-10-253-286-188	Sequence 188, App
22	10	37.0	17	16	US-10-809-689-11	Sequence 11, Appl
23	9	33.3	9	15	US-10-245-871-171	Sequence 171, App
24	9	33.3	9	15	US-10-253-286-171	Sequence 171, App
25	9	33.3	14	15	US-10-245-871-181	Sequence 181, App
26	9	33.3	14	15	US-10-253-286-181	Sequence 181, App
27	9	33.3	16	16	US-10-809-689-12	Sequence 12, Appl
28	7	25.9	7	8	US-08-464-363-65	Sequence 65, Appl
29	7	25.9	7	15	US-10-463-113-65	Sequence 65, Appl
30	7	25.9	62	14	US-10-029-386-29338	Sequence 29338, A
31	7	25.9	79	15	US-10-424-599-151766	Sequence 151766, A
32	7	25.9	106	16	US-10-437-963-199810	Sequence 199810, A
33	7	25.9	110	15	US-10-425-114-61756	Sequence 61756, A
34	7	25.9	132	15	US-10-425-114-66395	Sequence 66395, A
35	7	25.9	151	16	US-10-437-963-133298	Sequence 133298, A
36	7	25.9	169	16	US-10-425-115-212287	Sequence 212287, A
37	7	25.9	203	16	US-10-767-701-37074	Sequence 37074, A
38	7	25.9	246	16	US-10-425-115-304369	Sequence 304369, A
39	7	25.9	254	16	US-10-767-701-43856	Sequence 43856, A
40	7	25.9	317	18	US-10-450-763-32298	Sequence 32298, A
41	7	25.9	352	15	US-10-282-1224-59866	Sequence 59866, A
42	7	25.9	385	16	US-10-425-115-304368	Sequence 304368, A
43	7	25.9	455	15	US-10-369-493-18374	Sequence 18374, A
44	7	25.9	749	16	US-10-437-963-133292	Sequence 133292, A
45	7	25.9	990	16	US-10-437-963-170216	Sequence 170216, A

ALIGNMENTS

RESULT 1
US-10-295-903-4
; Sequence 4, Application US/10295903
; Publication No. US20030177512A1
GENERAL INFORMATION:
; APPLICANT: AVNER, David B.
; TITLE OF INVENTION: METHOD OF GENETICALLY ALTERING AND
; PRODUCING ALLERGY FREE CATS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/295,903
; FILING DATE: 18-JUN-2002
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,189
; FILING DATE: 09-JUN-1995
; APPLICATION NUMBER: US 08/657,905
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 09/227,873
; FILING DATE: 11-JAN-1999
ATTORNEY/AGENT INFORMATION:
; NAME: SIMKIN, Michele M.

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/
/   REGISTRATION NUMBER: 34,717
/   REFERENCE/DOCKET NUMBER: 40065/105
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (202)672-5300
/   TELEFAX: (202)672-5399
/   INFORMATION FOR SEQ ID NO: 4:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 107 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-295-903-4

Query Match      100.0%; Score 27; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.4e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSITKVNAITEPERT 27
DB      31 FFAVANGNELLDLSITKVNAITEPERT 57

RESULT 2
US-08-464-363-6
/   Sequence 6, Application US/08464363
/   Publication No. US20030035815A1
/   GENERAL INFORMATION:
/   APPLICANT: Rogers, Bruce L.
/   APPLICANT: Morgenstern, Jay
/   APPLICANT: Bond, Julian F.
/   APPLICANT: Garman, Richard D.
/   APPLICANT: Greenstein, Julia L.
/   APPLICANT: Kuo, Mei-chang
/   APPLICANT: Morville, Malcolm
/   TITLE OF INVENTION: RECOMBITOPE PEPTIDES
/   NUMBER OF SEQUENCES: 76
/   CORRESPONDENCE ADDRESS:
/   ADDRESSEE: Lahive & Cockfield
/   STREET: 60 State Street, Suite 510
/   CITY: Boston
/   STATE: MA
/   COUNTRY: USA
/   ZIP: 02109
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: ASCII TEXT
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/464,363
/   FILING DATE: 05-JUN-1995
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 07/807,529
/   FILING DATE: 13-DEC-1991
/   APPLICATION NUMBER: US 07/662,276
/   FILING DATE: 28-FEB-1991
/   APPLICATION NUMBER: US 07/431,565
/   FILING DATE: 03-NOV-1989
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Amy E. Mandragouras
/   REGISTRATION/DOCKET NUMBER: 36,207
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (617) 227-7400
/   INFORMATION FOR SEQ ID NO: 6:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 109 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: protein
US-08-464-363-6
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Query Match      100.0%; Score 27; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      31 FFAVANGNELLDLSITKVNAITEPERT 57

RESULT 3
US-09-847-208-98
/   Sequence 98, Application US/09847208
/   Publication No. US20030082190A1
/   GENERAL INFORMATION:
/   APPLICANT: Saxon, Andrew
/   APPLICANT: Zhang, Ke
/   APPLICANT: Zhu, Daocheng
/   APPLICANT: Zhang, Ke
/   TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
/   TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES
/   FILE REFERENCE: UC67.002A
/   CURRENT APPLICATION NUMBER: US/09/847,208
/   CURRENT FILING DATE: 2001-05-01
/   NUMBER OF SEQ ID NOS: 177
/   SOFTWARE: FastSeq for Windows Version 4.0
/   SEQ ID NO 98
/   LENGTH: 109
/   TYPE: PRT
/   ORGANISM: Felis silvestris catus (Cat)
US-09-847-208-98

Query Match      100.0%; Score 27; DB 10; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSITKVNAITEPERT 27
DB      31 FFAVANGNELLDLSITKVNAITEPERT 57

RESULT 4
US-10-245-871-136
/   Sequence 136, Application US/10245871
/   Publication No. US20030235594A1
/   GENERAL INFORMATION:
/   APPLICANT: HUMPHREYS, ROBERT
/   APPLICANT: XU, MINZHEN
/   TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
/   FILE REFERENCE: REH-2013
/   CURRENT APPLICATION NUMBER: US/10/245,871
/   CURRENT FILING DATE: 2003-01-09
/   PRIOR APPLICATION NUMBER: 10/197,000
/   PRIOR FILING DATE: 2002-07-17
/   PRIOR APPLICATION NUMBER: 09/396,813
/   PRIOR FILING DATE: 1999-09-14
/   NUMBER OF SEQ ID NOS: 905
/   SOFTWARE: PatentIn Ver. 2.1
/   SEQ ID NO 136
/   LENGTH: 109
/   TYPE: PRT
/   ORGANISM: Felis domesticus
US-10-245-871-136

Query Match      100.0%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSITKVNAITEPERT 27
DB      31 FFAVANGNELLDLSITKVNAITEPERT 57

RESULT 5
US-10-463-113-6
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Sequence 6, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Wei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-463-113-6

Query Match 100.0%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNVATEPERT 27
DB 31 FFAVANGNELLDLSLTKNVATEPERT 57

RESULT 6
US-10-253-286-136
Sequence 136, Application US/10253286
Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: II-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813

PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 136
LENGTH: 109
TYPE: PRT
ORGANISM: Felis domesticus
US-10-253-286-136

Query Match 100.0%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNVATEPERT 27
DB 31 FFAVANGNELLDLSLTKNVATEPERT 57

RESULT 7
US-10-809-689-32
Sequence 32, Application US/10809689
Publication No. US20040265342A1
GENERAL INFORMATION:
APPLICANT: Eric Potter Clarkson
TITLE OF INVENTION: Methods and compositions for desensitisation
FILE REFERENCE: 5538/1010
CURRENT APPLICATION NUMBER: US/10/809,689
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: PCT/GB99/00080
PRIOR FILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: GB/9800445.0
PRIOR FILING DATE: 1998-01-09
PRIOR APPLICATION NUMBER: GB/9820474.6
PRIOR FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32
LENGTH: 109
TYPE: PRT
ORGANISM: Felis catus
US-10-809-689-32

Query Match 100.0%; Score 27; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNVATEPERT 27
DB 31 FFAVANGNELLDLSLTKNVATEPERT 57

RESULT 8
US-08-464-363-9
Sequence 9, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Wei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-363-9

Query Match 96.3%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPER 26
DB 1 FFAVANGNELLDLSLTKNATEPER 26

RESULT 9
US-10-463-113-9
Sequence 9, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565

FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 742-4214
TELEFAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-463-113-9

Query Match 96.3%; Score 26; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPER 26
DB 1 FFAVANGNELLDLSLTKNATEPER 26

RESULT 10
US-08-464-363-39
Sequence 39, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-363-39

Query Match 96.3%; Score 26; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPER 26
DB 44 FFAVANGNELLDLSITKVNATEPER 69

RESULT 11
US-10-463-113-39
Sequence 39, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm

TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529

FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-463-113-39

Query Match 96.3%; Score 26; DB 15; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPER 26
DB 44 FFAVANGNELLDLSITKVNATEPER 69

RESULT 12
US-08-464-363-17
Sequence 17, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm

TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESS: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529

FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-363-17

Query Match 59.3%; Score 16; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPER 16
DB 6 FFAVANGNELLDLSITKVNATEPER 21

RESULT 13
US-10-463-113-17
Sequence 17, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm

QY 1 FFAVANGNELLDLSITKVNATEPER 26
DB 44 FFAVANGNELLDLSITKVNATEPER 69

```

; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,113
; FILING DATE: 16-Jun-2003
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-463-113-17

Query Match          59.3%; Score 16; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PFAVANGNELLDLSL 16
DB      6 PFAVANGNELLDLSL 21

RESULT 14
US-08-464-363-19
; Sequence 19, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-363-19

Query Match          55.6%; Score 15; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 LDLSITKYNATEPPER 26
DB      1 LDLSITKYNATEPPER 15

RESULT 15
US-10-463-113-19
; Sequence 19, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,113
; FILING DATE: 16-Jun-2003
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
```

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-463-113-19

Query Match 55.6%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 LDLSLTVNATEPPER 26
Db 1 LDLSLTVNATEPPER 15

Search completed: October 18, 2005, 14:01:48
Job time : 179 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 13:28:53 ; Search time 178 Seconds
(without alignments)
77.675 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27

Sequence: 1 FFAVANGNELLDLSLTAVNATEPERT 27

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	109	1	PEL2_FELCA
2	8	29.6	509	2	06R184
3	7	23.9	77	2	09K659
4	7	23.9	100	2	08K1B4
5	7	23.9	106	2	06ZDG2
6	7	23.9	134	2	06PYC6
7	7	23.9	134	2	06DMV1
8	7	23.9	198	2	09X302
9	7	23.9	250	1	BACR_HAHL54
10	7	23.9	255	2	06FCV6
11	7	23.9	273	2	06CPS8
12	7	23.9	279	2	P73885
13	7	23.9	303	2	064761
14	7	23.9	310	2	08KXR1
15	7	23.9	310	2	06EXX1
16	7	23.9	310	2	074P16
17	7	23.9	315	2	08A9W0
18	7	23.9	320	1	ALX_PHOIL
19	7	23.9	322	2	08LTP9
20	7	23.9	322	2	09AAV5
21	7	23.9	358	2	07MA28
22	7	23.9	420	1	HIS2_STNP7
23	7	23.9	428	2	06CUA1
24	7	23.9	434	2	07XQ04
25	7	23.9	455	2	09CHP3
26	7	23.9	502	2	084ZD1
27	7	23.9	524	2	009012
28	7	23.9	524	2	07SW4
29	7	23.9	525	2	06VWU4
30	7	23.9	525	2	06VWU5
31	7	23.9	525	2	06VWU6

32	7	25.9	539	2	06FV10	06FV10 candida gla
33	7	25.9	552	2	06FQW2	06FQW2 candida gla
34	7	25.9	1595	2	07UG94	07UG94 rhodospirillum
35	7	25.9	1601	2	08IC14	08IC14 plasmidium
36	6	22.2	23	2	09H4H9	09H4H9 homo sapien
37	6	22.2	64	2	08HSD6	08HSD6 oryza sativ
38	6	22.2	86	2	073910	073910 human immun
39	6	22.2	86	2	073911	073911 human immun
40	6	22.2	86	2	073912	073912 human immun
41	6	22.2	87	2	09PDS8	09PDS8 xyloella fas
42	6	22.2	88	2	06Q214	06Q214 candidatus
43	6	22.2	91	2	09LRB3	09LRB3 nicotiana t
44	6	22.2	96	2	08EUV5	08EUV5 oceanobacill
45	6	22.2	97	2	09FVJ7	09FVJ7 nicotiana o

ALIGNMENTS

RESULT 1
PEL2_FELCA STANDARD; PRT; 109 AA.
ID PEL2_FELCA
AC P30440;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B)
DE (Fel d 1-B) (Allergen Cat-1) (Ag4) (Fdi).
GN Name=CH2;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-100.
RX MEDLINE=92052157; PubMed=1946388;
RA Morgenstern J.P., Griffith I.J., Brauer A.W., Rogers B.L., Bond J.F.,
RA Chapman M.D., Kuo M.-C.;
RT "amino acid sequence of Fel d1, the major allergen of the domestic
cat: protein sequence analysis and cDNA cloning."
RL Proc. Natl. Acad. Sci. U.S.A. 88:9690-9694(1991).
RN [2]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.
RC TISSUE=Liver;
RX MEDLINE=92241678; PubMed=1572548; DOI=10.1016/0378-1119(92)90405-E;
RA Griffith I.J., Craig S., Pollock J., Yu X.-B., Morgenstern J.P.,
RA Rogers B.L.;
RT "Expression and genomic structure of the genes encoding Fdi, the major
allergen from the domestic cat."
RL Gene 113:263-268(1992).
RN [3]
RP SEQUENCE OF 18-37, AND CHARACTERIZATION.
RX MEDLINE=91287714; PubMed=1712068; DOI=10.1016/0161-5890(91)90141-6;
RA Duffort O.A., Carreira J., Nicli G., Polo F., Lombardero M.;
RT "Studies on the biochemical structure of the major cat allergen Fells
domesticus I."
RL Mol. Immunol. 28:301-309(1991).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=84265679; PubMed=6747135;
RA Leterman K., Ohman J.L. Jr.;
RT "Cat allergen I: biochemical, antigenic, and allergenic properties."
RL J. Allergy Clin. Immunol. 74:147-153(1984).
CC -1- SUBUNIT: Heterotetramer composed of two non-covalently linked
disulfide-linked heterodimer of chains 1 and 2.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
isoforms;
Name=1; Synonyms=CH2L;
Isoid=P30440-1; Sequence=Displayed;
Name=2; Synonyms=CH2S;
Isoid=P30440-2; Sequence=VSP_004249;

```

CC Name=3; Synonyms=CH2ST. Truncated:
CC IsoId=D30440-3; Sequence=VSP_004248;
CC TISSUE SPECIFICITY: The long form is preferentially expressed in
CC the salivary gland, while the short form is preferentially
CC expressed in the skin.
CC -I ALLERGEN: Causes an allergic reaction in human. Major allergen
CC produced by the domestic cat.
-----
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CC or send an email to license@isb-sib.ch) .
CC
DR EMBL; M77341; AAC41516.1; -.
DR EMBL; X62478; CAA43445.1; -.
DR PIR; B53283; B53283.
DR PIR; C56413; C56413.
DR PIR; JCL127; JCL127.
DR InterPro; IPR006038; Uteroglobulin supf.
KM Allergen; Alternative splicing; Direct protein sequencing;
KW Glycoprotein; Polymorphism; Signal.
FT SIGNAL 1 17
FT CHAIN 18 109 Major allergen I polypeptide chain 2.
FT CARBOHYD 50 50 N-linked (GlcNAc...)
FT VASPLIC 82 109 TTISSKKMGGEAVNTVEDTKNLTGR -> PSTNIAMVK
FT OPRP (in isoform 3).
FT FTID=VSP_004248.
FT TTSSSKD -> IATNEY (in isoform 2).
FT VASPLIC 82 89 FTID=VSP_004249.
FT VARIANT 72 72 I -> L ((in CH2LV)).
FT VARIANT 72 72 I -> V ((in CH2SV)).
FT VARIANT 74 75 RV -> KP ((in CH2SV)).
FT VARIANT 91 91 M -> T ((in CH2LV)).
FT VARIANT 96 96 Q -> E ((in CH2SV)).
FT VARIANT 105 105 N -> K ((in CH2SV)).
FT CONFLICT 24 24 C -> F (in Ref. 3).
FT CONFLICT 32 32 F -> T (in Ref. 3).
SQ SEQUENCE 109 AA; 11854 MW; 857FB9CD76036CB9 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 1 FFVAANGNELLDLSITRYNATEPERT 27
Db 31 FFVAANGNELLDLSITRYNATEPERT 57

RESULT 2
ID O6R184 PRELIMINARY; PRT; 509 AA.
AC O6R184;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE PAR1 proteain (Fragment).
GN Name=PAR1;
OS Zygosaccharomyces rouxi (Candida mogii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
CX NCBI_TaxID=4956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 732;
RL Wolfe R.H.;
RL Submitted (DEC-2003) to the EMBL/genbank/DDJB databases.
DR EMBL; AY496963; AAR88365.1; -.
FT NON TER 509 AA; 58713 MW; BAB6F2FBAE901589 CRC64;
SQ SEQUENCE 509 AA; 58713 MW; BAB6F2FBAE901589 CRC64;
```

Query Match	Similarity	100.0%	Score 8:	DB 2:	Length 509:
Best Local	Similarity	100.0%	Pred. No. 8.8:		
Matches	8:	Conservative	0:	Mismatches	0:
				Indels	0:
				Gaps	0:
OY	7 GNEILLDL 14				
DB	54 ELLLDL 61				
RESULT 3					
O9KG69	PRELIMINARY;	PRT;	77 AA.		
AC	O9KG69;				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE	BH0244 protein.				
GN	OrderedLocusNames=BH0244;				
OS	Bacillus halodurans.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_Taxid=86665;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C-125.				
RA	MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;				
RA	Takami H., Nakaone K., Takaki Y., Maeno G., Sasaki R., Masui N.,				
RA	Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,				
RA	Horikoshi K.;				
RT	"Complete genome sequence of the alkaliphilic bacterium Bacillus				
RT	halodurans and genomic sequence comparison with Bacillus subtilis."				
RL	Nucleic Acids Res. 28:4317-4331(2000).				
DR	EMBL; AP001507; BAB03963.1; -.				
DR	PIR; D83680; D83680.				
KV	Complete proteome.				
SEQ	SEQUENCE 77 AA; 9511 MW; F9BEC3529F5CE320 CRC64;				
Query Match	Similarity	25.9%	Score 7:	DB 2:	Length 77:
Best Local	Similarity	100.0%	Pred. No. 17:		
Matches	7:	Conservative	0:	Mismatches	0:
				Indels	0:
				Gaps	0:
OY	9 ELLLDL 15				
DB	24 ELLLDL 30				
RESULT 4					
O8KLB4	PRELIMINARY;	PRT;	100 AA.		
ID	O8KLB4				
AC	O8KLB4;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE	Hypothetical protein yH014.				
GN	Name=yH014;				
OS	Rhizobium etl.				
OC	Plasmid symbiotic plasmid p42d.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.				
OX	NCBI_Taxid=29449;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CFN42;				
RX	MEDLINE=91193195; PubMed=2013564;				
RA	Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;				
RT	"Structural complexity of the symbiotic plasmid of Rhizobium				
RT	leguminosarum bv. phaseoli."				
RL	J. Bacteriol. 173:2411-2419(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CFN42;				
RX	MEDLINE=97419521; PubMed=9274036;				
RA	Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,				
RA	Cevallos M.A., Davila G.;				


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RT efflux gene mef(A) in Streptococcus pyogenes.";
RL Microb. Drug Resist. 9:243-247(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2812A;
RA Santagati M., Iannelli F., Cascone C., Stefani S., Pozzi G.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF657002; AAT72374.1; -.
KW Hypothetical protein.
SQ SEQUENCE 134 AA; 15373 MW; 897916A18372A242 CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 2; Length 134;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 11 LLDLST 17
DB 25 LLDLST 31

RESULT 8
O9X302 PRELIMINARY; PRT; 198 AA.
ID O9X302;
AC O9X302;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DE PX01-31.
OS Bacillus anthracis.
OC Plasmid virulence plasmid PX01.
OC Bacteri; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OK NCBI_TaxId=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne;
RX MEDLINE=99445463; PubMed=10515943;
RA Okinaka R.T., Cloud K., Hampton O., Hofmeister A.R., Hill K.K.,
RA Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
RA Martinez Y., Riche D., Svensson R., Jackson P.J.;
RT "Sequence and organization of PX01, the large Bacillus anthracis
RT plasmid harboring the anthrax toxin genes.";
RL J. Bacteriol. 181:6509-6515(1999).
RW EMBL; AF065404; AAD3235.1; -.
DR PIR; G59094; G59094.
KW Plasmid.
SQ SEQUENCE 198 AA; 22859 MW; D76737FD81C43C9D CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 2; Length 198;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 8 NEBLDL 14
DB 150 NEBLDL 156

RESULT 9
BACR HALS4 STANDARD; PRT; 250 AA.
ID BACR HALS4;
AC O93740;
DT 16-OCT-2001 (REL. 40, Created)
DT 16-OCT-2001 (REL. 40, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Bacteriorhodopsin (BR).
GN Name=brp;
OS Halobacterium sp. (strain arg-4).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OK NCBI_TaxId=160432;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9906913; PubMed=878396; DOI=10.1006/jmbi.1998.2286;
RT Ihara K., Umemura T., Katagiri I., Kitajima-Ihara T., Sugiyama Y.,

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RA Kimura Y., Mukohata Y.;
RT "Evolution of the archael rhodopsins: evolution rate changes by gene
RT duplication and functional differentiation.";
RL J. Mol. Biol. 285:163-174(1999).
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2812A;
RA Santagati M., Iannelli F., Cascone C., Stefani S., Pozzi G.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF657002; AAT72374.1; -.
KW Hypothetical protein.
SQ SEQUENCE 134 AA; 15373 MW; 897916A18372A242 CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 2; Length 250;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 10 LLDLST 16
DB 101 LLDLST 107

RESULT 10
O6FCV6 PRELIMINARY; PRT; 255 AA.
ID O6FCV6;
AC O6FCV6;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Survival protein (acid phosphatase) (EC 3.1.3.2).
GN Name=surv; OrderedLocNames=ACTAD1227;
OS Actinobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Actinobacter.
OK NCBI_TaxId=62977;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9906913; PubMed=878396; DOI=10.1006/jmbi.1998.2286;
RT Ihara K., Umemura T., Katagiri I., Kitajima-Ihara T., Sugiyama Y.,

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RL Nucleic Acids Res. 0:0-0(2004).
 DR EMBL; CR543861; CAG68103.1; -.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR002828; SURF.
 DR Pfam; PF01975; SURF.1.
 DR ProDom; PD005378; SURF.1.
 DR TrRfam; TRFR00087; SURF.1.
 DR Complete proteome.
 SO SEQUENCE 255 AA; 27574 MW; CAFE04235EP82A46 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVANG 7
 Db 224 FAVANG 230

RESULT 11
 ID 06CP58 PRELIMINARY; PRT; 273 AA.
 AC 06CP58;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|P26754|Saccharomyces cerevisiae YNL312w RFA2 DNA replication factor A.
 GN ORFNames=K1LA0B0734Bg;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NC NCBI_TaxId=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., March C., Neuvéglise C., Talla E., Goffard N., Frangul L., Aigle M., Anthouard V., Bahour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Catolico L., Confiantoli F., de Daruvar A., Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppl A., Hantave F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J., Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; G3382125; CAG9368.1; -.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR004365; tRNA anti.
 DR Pfam; PF01336; tRNA anti.1.
 SO SEQUENCE 273 AA; 30347 MW; 4121F346314942BD CRC64;

Query Match 25.9%; Score 7; DB 2; Length 273;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FAVANG 8
 Db 174 FAVANG 180

RESULT 12
 ID P73885 PRELIMINARY; PRT; 279 AA.
 AC P73885;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE S1r0267 protein.
 GN OrderedLocNames=S1r0267;
 OS Synchocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
 NC NCBI_TaxId=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T., Hosouchi T., Matsuo A., Muraki A., Nakazaki N., Nario K., Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90910; BAA17949.1; -.
 DR PIR; S75087; S75087.
 DR HSR1; 031743; 1PUY.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR005289; GTP-binding.
 DR InterPro; IPR006073; GTP_OBG.
 DR InterPro; IPR002917; MMR_HSR1.
 DR Pfam; PF01926; MMR_HSR1.1.
 DR PRINTS; PR00326; GTP_OBG.
 DR TrRfam; TRFR00650; MGA442.1.
 SO SEQUENCE 279 AA; 31201 MW; 9AA60F311BD77763 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LLLDLSL 16
 Db 213 LLLDLSL 219

RESULT 13
 ID 064761 PRELIMINARY; PRT; 303 AA.
 AC 064761;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative phosphatidylinositol-glycan synthase.
 GN Name=At2g34980;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rounselle S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004238; AAC12837.1; -.

DR PIR; T00479; T00479.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0017176; F:phosphatidylinositol N-acetylglucosaminyltr. .; IEA.
 DR GO; GO:0006506; P:GPI anchor biosynthesis; IEA.
 DR InterPro; IPR009450; GPI2.
 DR Pfam; PF06432; GPI2; 1.
 SQ SEQUENCE 303 AA; 34200 MW; 88EBF82F4940C92 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLLDLSL 16
 |||||
 DB 89 NLLDLSL 95

RESULT 14

08KXR1 PRELIMINARY; PRT; 310 AA.
 ID 08KXR1
 AC 08KXR1; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein BXA0045.
 GN Name=BXA0045;
 OS Bacillus anthracis str. A2012.
 OG Plasmid PX01.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_Taxid=191218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A2012;
 RC MEDLINE=22061436; PubMed=12004073; DOI=10.1126/science.1071837;
 RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
 RA Holtzapfel E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
 RA Keim P., Fraser C.M.;
 RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
 RT Bacillus anthracis.";
 RT Science 296:2028-2033(2002).
 DR EMBL; AE011190; AAM26001.1; -.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 310 AA; 36423 MW; 716F21DB64CFE274 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NLLDLSL 14
 |||||
 DB 262 NLLDLSL 268

RESULT 15

06EZXL PRELIMINARY; PRT; 310 AA.
 ID 06EZXL
 AC 06EZXL; 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=GBAA_PX01_0045;
 OS Bacillus anthracis.
 OG Plasmid PX01.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_Taxid=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics.";

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017336; AAT28786.2; -.
 DR TIGR; GBAA_PX01_0045; -.
 KW Complete proteome.
 SQ SEQUENCE 310 AA; 36423 MW; 716F21DB64CFE274 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NLLDLSL 14
 |||||
 DB 262 NLLDLSL 268

Search completed: October 18, 2005, 13:47:25
 Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:37:20 ; Search time 39 Seconds
(without alignments)
66.612 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27
Sequence: 1 FFAVANGNELLDLSITKVNAITEPERT 27

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	107	2 JC1127	major allergen cha
2	27	100.0	109	2 C56413	major allergen Fel
3	27	100.0	107	2 D83680	hypothetical prote
4	27	100.0	107	2 D83680	hypothetical prote
5	27	100.0	107	2 D83680	hypothetical prote
6	27	100.0	107	2 D83680	hypothetical prote
7	27	100.0	107	2 D83680	hypothetical prote
8	27	100.0	107	2 D83680	hypothetical prote
9	27	100.0	107	2 D83680	hypothetical prote
10	27	100.0	107	2 D83680	hypothetical prote
11	27	100.0	107	2 D83680	hypothetical prote
12	27	100.0	107	2 D83680	hypothetical prote
13	27	100.0	107	2 D83680	hypothetical prote
14	27	100.0	107	2 D83680	hypothetical prote
15	27	100.0	107	2 D83680	hypothetical prote
16	27	100.0	107	2 D83680	hypothetical prote
17	27	100.0	107	2 D83680	hypothetical prote
18	27	100.0	107	2 D83680	hypothetical prote
19	27	100.0	107	2 D83680	hypothetical prote
20	27	100.0	107	2 D83680	hypothetical prote
21	27	100.0	107	2 D83680	hypothetical prote
22	27	100.0	107	2 D83680	hypothetical prote
23	27	100.0	107	2 D83680	hypothetical prote
24	27	100.0	107	2 D83680	hypothetical prote
25	27	100.0	107	2 D83680	hypothetical prote
26	27	100.0	107	2 D83680	hypothetical prote
27	27	100.0	107	2 D83680	hypothetical prote
28	27	100.0	107	2 D83680	hypothetical prote
29	27	100.0	107	2 D83680	hypothetical prote

30	6	22.2	201	2 S76151	hypothetical prote
31	6	22.2	210	1 ISVKNT	phosphoribosylanth
32	6	22.2	226	2 T30615	hypothetical prote
33	6	22.2	227	2 D71312	probable Holliday
34	6	22.2	229	2 S57957	thrombospondin 1 -
35	6	22.2	230	1 UN0060	hypothetical 24.5K
36	6	22.2	237	2 D83969	RNA polymerase spo
37	6	22.2	237	2 F70606	probable pkmw spo
38	6	22.2	238	2 H95105	pillin gene inverti
39	6	22.2	239	1 B39441	transcription init
40	6	22.2	239	1 U00083	transcription init
41	6	22.2	240	2 S75462	hypothetical prote
42	6	22.2	240	2 T20791	hypothetical prote
43	6	22.2	246	2 S19193	hypothetical prote
44	6	22.2	246	2 T20792	hypothetical prote
45	6	22.2	249	2 AH2152	hypothetical prote

ALIGNMENTS

RESULT 1

JC1127

major allergen chain 2 precursor, short form - cat

C:Species: Felis silvestris catus (domestic cat)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: JC1127

R:Griffith, I.J.; Craig, S.; Pollock, J.; Yu, X.B.; Morgenstern, J.P.; Rogers, B.L.

Gene 113, 263-268, 1992

A>Title: Expression and genomic structure of the genes encoding Fd1, the major allergen

A/Reference number: JC1126; MUID:92241678; PMID:1572548

A/Accession: JC1127

A/Molecule type: DNA

A/Residues: 1-107 <GRL>

A/Cross-references: UNIPROT:P30440; GB:X62478; NID:9395406; PIDN:CAA44345.1; PID:9395407

A/Experimental source: skin

C/Genetics:

A:Gene: Ch2

A:Introns: 21/1; 81/3

C/Keywords: glycoprotein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-107/Product: major allergen chain 2, short form #status predicted <MAT>

F:50/Banding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNAITEPERT 27

DB 31 FFAVANGNELLDLSITKVNAITEPERT 57

RESULT 2

C56413

major allergen Fel di chain 2 precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C/Accession: C56413; JC1145

R:Morgenstern, J.P.; Griffith, I.J.; Brauer, A.W.; Rogers, B.L.; Bond, J.F.; Chapman, M

Proc. Natl. Acad. Sci. U.S.A. 88, 9690-9694, 1991

A>Title: Amino acid sequence of Fel d1, the major allergen of the domestic cat: protein

A/Reference number: A56413; MUID:92052157; PMID:1946388

A/Accession: C56413

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-109 <MOB>

A/Cross-references: UNIPROT:P30440; GB:M77341; NID:9163822; PIDN:AA41616.1; PID:9163823

R:Griffith, I.J.; Craig, S.; Pollock, J.; Yu, X.B.; Morgenstern, J.P.; Rogers, B.L.

Gene 113, 263-268, 1992

A>Title: Expression and genomic structure of the genes encoding Fd1, the major allergen

A/Reference number: JC1126; MUID:92241678; PMID:1572548

A/Accession: JC1145

A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 18-109 <GR>

A:Experimental source: salivary gland

C:Keywords: glycoprotein

F1-1//Domain: signal sequence #status predicted <Sig>

F150/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27

DB 31 FFAVANGNELLDLSITKVNATEPERT 57

RESULT 3

DB3680

hypothetical protein BH0244 [imported] - *Bacillus anthracis* virulence plasmid pXOI

C:Species: *Bacillus anthracis*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: D83680

R:Takekuni, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliophilic bacterium *Bacillus halodurans* and

A:Reference number: AB3650; MUID:20512582; PMID:11058132

A:Accession: D83680

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <STO>

A:Cross-references: UNIPROT:Q9KG69; GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA8039

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0244

Query Match 25.9%; Score 7; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ELLLDLS 15

DB 24 ELLLDLS 30

Query Match 25.9%; Score 7; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ELLLDLS 15

DB 24 ELLLDLS 30

RESULT 4

GS9094

hypothetical protein pXOI-31 - *Bacillus anthracis* virulence plasmid pXOI

C:Species: *Bacillus anthracis*

C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C:Accession: G59094

R:Okimura, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler

J. Bacteriol. 181, 6509-6515, 1999

A:Title: Sequence and organization of pXOI, the large *Bacillus anthracis* plasmid harbored

A:Reference number: A59091; MUID:99445463; PMID:10515943

A:Accession: G59094

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-198 <OKI>

A:Cross-references: UNIPROT:Q9X302; GB:AF065404; NID:G4694216; PIDN:AAD3235.1; PID:G469

A:Experimental source: strain Sterne

C:Genetics:

A:Gene: pXOI-31

A:Genome: plasmid

C:Superfamily: *Bacillus anthracis* virulence plasmid pXOI hypothetical protein pXOI-31

Query Match 25.9%; Score 7; DB 2; Length 198;

Best Local Similarity 100.0%; Pred. No. 7.3;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NELLIDL 14

DB 150 NELLIDL 156

RESULT 5

T50677

bacteriorhodopsin [similarity] - "*Haloterrigena*" sp. (strain arg-4)

C:Species: "*Haloterrigena*" sp.

A:Variety: strain arg-4

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000

C:Accession: T50677

R:Iihara, K.; Umemura, T.; Katagiri, I.; Kitajima-Iihara, T.; Sugiyama, Y.; Kimura, Y.; Mu

J. Mol. Biol. 285, 163-174, 1999

A:Title: Evolution of the archaean rhodopsin: Evolution rate changes by gene duplicatio

A:Reference number: 222703; MUID:99096913; PMID:9878396

A:Accession: T50677

A>Status: preliminary

A:Molecule type: DNA

A:Cross-references: EMBL:AB009620; PIDN:BA75200.1

C:Genetics:

A:Gene: bop

C:Superfamily: bacteriorhodopsin

C:Keywords: chromoprotein; photoreceptor; retinal; transmembrane protein

F1225/Binding site: retinal (Lys) (covalent) #status predicted

Query Match 25.9%; Score 7; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDLSL 16

DB 101 LLLDLSL 107

RESULT 6

S75087

hypothetical protein slr0267 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S75087

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75087

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-279 <KAN>

A:Cross-references: UNIPROT:P73685; EMBL:D90910; GB:AB001339; NID:G1652956; PIDN:BA1794

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: conserved hypothetical protein MG442

Query Match 25.9%; Score 7; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDLSL 16

DB 213 LLLDLSL 219

RESULT 7

T00479

probable phosphatidylinositol-glycan synthase [imported] - *Arabidopsis thaliana*

N:Alternate names: hypothetical protein F1913.21

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00479; B84763

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau

submitted to the EMBL Data Library, April 1998

A:Description: *Arabidopsis thaliana* chromosome II BAC F1913 genomic sequence.

A:Reference number: 214160
 A:Accession: T00479
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-303 <R0U>
 A:Cross-references: UNIPROT:064761; EMBL:AC004238; NID:G3033373; PID:G3033393
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euse, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:1061197
 A:Accession: B84763
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-303 <STO>
 A:Cross-references: GB:AE002093; NID:G3033393; PIDN:AA012837.1; GSPDB:GN00139
 A:Genetics:
 A:Gene: ATG34980; F1913.21
 A:Map position: 2

Query Match 25.9%; Score 7; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LITVNST 16
 |||||
 DB 89 LITVNST 95

RESULT 8
 B86722
 biotin carboxylase (EC 6.3.4.14) [imported] - Lactococcus lactis subsp. lactis (strain I
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B86722
 R:Bojocin, A.; Winkler, P.; Mauger, S.; Jallou, O.; Malarme, K.; Weissbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: B86722
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-455 <STO>
 A:Cross-references: UNIPROT:Q9CHF3; GB:AE005176; PID:G12723697; PIDN:AAK04876.1; GSPDB:G
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: accC
 C:Superfamily: biotin carboxylase; biotin carboxylase homology
 C:Keywords: ligase

Query Match 25.9%; Score 7; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VANGNEL 10
 |||||
 DB 316 VANGNEL 322

RESULT 9
 S44982
 flagellin - *Shigella sonnei*
 C:Species: *Shigella sonnei*
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S44982; S44981
 R:Tomimaga, A.; Mahmoud, M.A.H.; Mukaihara, T.; Enomoto, M.
 Mol. Microbiol. 12, 277-285, 1994
 A:Title: Molecular characterization of intact, but cryptic, flagellin genes in the genus
 A:Reference number: S44980; MUID:94335647; PMID:8057852
 A:Accession: S44982
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-524 <TOM>
 A:Cross-references: UNIPROT:Q09012; EMBL:D16821; NID:G391893; PIDN:BAA04095.1; PID:G39185
 C:Superfamily: flagellin

Query Match 25.9%; Score 7; DB 2; Length 524;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LITVNST 22
 |||||
 DB 196 LITVNST 202

RESULT 10
 B82678
 hypothetical protein XFI461 [imported] - *Xylella fastidiosa* (strain 945c)
 C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: B82678
 R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: B82678
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-87 <SIM>
 A:Cross-references: UNIPROT:Q9PDB8; GB:AE003976; GB:AE003849; NID:G9106479; PIDN:AAE9427
 A:Experimental source: strain 945c
 R:Simpton, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.; A
 Brixton, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H
 as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigt
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Mircea, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
 M.; Tashko, M.H.; Vallada, H.; Van Sluyt, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 A:Genetics:
 C:Genetics:
 A:Gene: XFI461

Query Match 22.2%; Score 6; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 NEILD 13
 |||||
 DB 2 NEILD 7

RESULT 11
 E90093
 hypothetical protein orf100 [imported] - *Gulliardia theta* nucleomorph
 C:Species: nucleomorph *Gulliardia theta*
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: E90093
 R:Douglas, S.; Zauner, S.; Pirmaholiz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re
 Nature 410, 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: E90093
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-100 <DOU>
 A:Cross-references: UNIPROT:Q98R80; GB:AF165818; NID:G13794502; PIDN:AAK39877.1; GSPDB G

C/Genetics:
A/Gene: orf100
A/Map position: 1
A/Genome: nucleomorph
C/Keywords: nucleomorph

Query Match	22.2%	Score 6;	DB 2;	Length 100;
Best Local Similarity	100.0%	Pred. No. 41;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
Qy	10	LLDDLS	15	
Db	40	LLDDLS	45	

RESULT 12
KIRTA

Ig kappa chain C region (allele a) - rat
C:Species: Rattus norvegicus (Norway rat)

C/Date: 18-Aug-1982 #sequence_revision 10-Sep-1982
C/Accession: A02118
R/Sheppard, H.W.; Guttman, G.A.
R/Accession: 18-Aug-1982 #sequence_revision 10-Sep-1982

Proc. Natl. Acad. Sci. U.S.A. 78, 1064-1068, 1981

A1: Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the I kappa locus

A1: Reference number: A93901, PMID:82082587, PMID:6273908

A1: Keywords: kappa chain; I kappa locus; selection; allelic forms; rat

A1: Accession: A02410
A1: Molecule type: DNA
A1: Residues: 1-106 <SHE>
A1: Cross-references: INSDC, D0195C, CB, T09574, CB, T0074E, MTD, C0204820, STDN, B0041011 1-

CComplex: An immunoglobulin heterotetramer subunit consists of two identical light (*kappa*) chains and two heavy chains, each with a variable domain and a constant domain. The amino acid sequence of the heavy chain is: UNIKLHLEFVLSQD; GB:U000743; NID:G205820; FIDN:A06441411.L
AExperimental source: strain DA
CComplex: An immunoglobulin heterotetramer subunit consists of two identical light (*kappa*) chains and two heavy chains, each with a variable domain and a constant domain. The amino acid sequence of the heavy chain is: UNIKLHLEFVLSQD; GB:U000743; NID:G205820; FIDN:A06441411.L

C; Superfamily: immunoglobulin C region; immunoglobulin homology domain
C; Keywords: heterotetramer
E: 19-88/Domain: immunoglobulin homology; α -TM
C; Keywords: heterotetramer

```

Query Match      22.2%  Score 6;  DB 1;  length 106;
Best Local Similarity 100.0%  Pred. No. 43;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0
P:106/Disulfide bonds: interchain (to heavy chain) #status predicted

```

Qy	14	LSLTKV	19
Db	71	LSLTKV	76

Hypothetical protein APE1252 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #last change 09-Jul-2004

ClAccession: D72598
C1: Kawatabayashi, Y.; Hino, Y.; Hotikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takahara, H.; Takami, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, T.; K

DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: D72598
A:Status: preliminary
A:Molecule type: DNA

Query Match	Score	DB	Length
A:Residues: 1-107 <KAM> A:Cross-references: UNIPROT:Q9YCK5; DDBJ:AP000061; NID:gs104821; PIDD:BAAB0242.1; PID:ds104821	22.2%	6	107
A:Experimental source: strain KL C:GeneticCB: A:Gene: APE1252			

Db 84 NATEPE 89

RESULT 14

T09060
hypothetical protein NG1 - mouse
C1:Species: Mus musculus (house mouse)

```
CjDate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Jul-2004
CjAccession: T09060
RjRowen, L.; Mahatir, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
RjRowen, L.; Mahatir, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
RjRowen, L.; Mahatir, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
```

Submitted to the Embryo Data Library, October 1997.
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
Accession: M00060

A1Accession: U03060
A1Status: preliminary; translated from GB/EMBL/DBJ
A1Molecule type: DNA
A1Restriction: 1-112 (POM)

A:Accession: [U0112](#)
 A:Cross-references: UNIPROT:Q35443; EMBL:AF030001; NID:g2564945; PID:g2564948
 C:Genetics:
 A:Gene: NG1

```

A;Map position: 17
A;Introns: 13/3; 67/3

Query Match      22.2%; Score 6; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Oy	9	ELIIDL	14
Db	15	ELIIDL	20

RESULT 15

490453

hypothetical protein SSO2777 [imported] - *Sulfolobus solfataricus*
 #Species: *Sulfolobus solfataricus*
 C.Date: 24-May-2001 #sequence revision 24-May-2001 #text change 09-Jul-2004

C/Accession: H90453
R. Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Rishe, I.; Jeffries, A.C.; Kozera, N.; Penn, X.; Thi-NGoc, H.P.; Redder, P.
Jong, I.; Jeffries, A.C.; Kozera, N.; Penn, X.; Thi-NGoc, H.P.; Redder, P.

arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
.;Description: *Sulfolobus solfataricus* complete genome.

A;Reference number: A99139
A;Accession: H90453
A;Status: preliminary

Query Match	Score	DB	Length
A: Molecule type: DNA A: Residues: 1-118 <KDR> A: Cross-references: UNIPROT:Q9TVS8; GB:AB06641; NID:G13B16114; PIDN:AAK42687.1; GSPDB:C; C: Gene: S802777	22.28	6	118

```

QY      7 GNEILL 12      |||||
Db      21 GNEILL 26      |||||

Search completed: October 18, 2005, 13:48:10
Job time : 42 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:38:43 ; Search time 42 Seconds
(without alignments)
47.989 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27

Sequence: 1 PFAVANGNELLDLSLTKNATEPERT 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	90	3 US-08-300-928C-14	Sequence 14, Appl
2	27	100.0	90	3 US-08-430-944D-14	Sequence 14, Appl
3	27	100.0	90	3 US-08-430-014-14	Sequence 14, Appl
4	27	100.0	90	3 US-08-431-184-14	Sequence 14, Appl
5	27	100.0	92	3 US-08-300-928C-13	Sequence 13, Appl
6	27	100.0	92	3 US-08-430-944D-13	Sequence 13, Appl
7	27	100.0	92	3 US-08-430-014-13	Sequence 13, Appl
8	27	100.0	92	3 US-08-431-184-13	Sequence 13, Appl
9	27	100.0	97	3 US-08-300-928C-10	Sequence 10, Appl
10	27	100.0	97	3 US-08-430-944D-10	Sequence 10, Appl
11	27	100.0	97	3 US-08-430-014-10	Sequence 10, Appl
12	27	100.0	97	3 US-08-431-184-10	Sequence 10, Appl
13	27	100.0	109	1 US-07-662-193-5	Sequence 5, Appl
14	27	100.0	109	1 US-07-807-529A-6	Sequence 6, Appl
15	27	100.0	109	3 US-08-300-928C-8	Sequence 8, Appl
16	27	100.0	109	3 US-08-430-944D-8	Sequence 8, Appl
17	27	100.0	109	3 US-08-430-014-8	Sequence 8, Appl
18	27	100.0	109	3 US-08-431-184-8	Sequence 8, Appl
19	27	100.0	109	5 PCT-US93-02462-6	Sequence 6, Appl
20	27	100.0	111	1 US-07-662-193-4	Sequence 4, Appl
21	27	100.0	111	3 US-08-300-928C-6	Sequence 6, Appl
22	27	100.0	111	3 US-08-430-944D-6	Sequence 6, Appl
23	27	100.0	111	3 US-08-430-014-6	Sequence 6, Appl
24	27	100.0	111	3 US-08-431-184-6	Sequence 6, Appl
25	26	96.3	26	1 US-07-807-529A-9	Sequence 9, Appl
26	26	96.3	26	3 US-08-300-928C-19	Sequence 19, Appl
27	26	96.3	26	3 US-08-430-944D-19	Sequence 19, Appl

28	26	96.3	26	3 US-08-430-014-19	Sequence 19, Appl
29	26	96.3	26	3 US-08-431-184-19	Sequence 19, Appl
30	26	96.3	26	5 PCT-US93-02462-9	Sequence 9, Appl
31	26	96.3	96	1 US-07-807-529A-39	Sequence 39, Appl
32	26	96.3	96	3 US-08-430-944D-103	Sequence 103, App
33	26	96.3	96	3 US-08-431-184-103	Sequence 103, App
34	26	96.3	96	3 US-08-300-928C-16	Sequence 16, Appl
35	19	70.4	82	3 US-08-430-944D-16	Sequence 16, Appl
36	19	70.4	82	3 US-08-430-014-16	Sequence 16, Appl
37	19	70.4	82	3 US-08-431-184-16	Sequence 16, Appl
38	19	70.4	83	1 US-07-662-193-7	Sequence 7, Appl
39	19	70.4	83	1 US-07-662-193-8	Sequence 8, Appl
40	18	66.7	18	3 US-08-300-928C-25	Sequence 25, Appl
41	18	66.7	18	3 US-08-430-944D-25	Sequence 25, Appl
42	18	66.7	18	3 US-08-430-014-25	Sequence 25, Appl
43	18	66.7	18	3 US-08-431-184-25	Sequence 25, Appl
44	18	66.7	27	3 US-08-300-928C-57	Sequence 57, Appl
45	18	66.7	27	3 US-08-430-944D-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-08-300-928C-14
Sequence 14, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEPTER, Malcolm J., et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-14
Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 FFAVANGNELLDLSITKVNATEPERT 40

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RESULT 2
US-08-430-944D-14
; Sequence 14, Application US/08430944D
; Patent No. 6025162
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-430-944D-14

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
Db 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 3
US-08-430-014-14
; Sequence 14, Application US/08430014
; Patent No. 6048962
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
```

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/ COUNTRY: USA
/ ZIP: 02145
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/430,014
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/300,928
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: AMY E. MANDRAGOURAS
/ REGISTRATION NUMBER: 36,207
/ REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 90 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ US-08-430-014-14
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Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
Db 14 FFAVANGNELLDLSITKVNATEPERT 40

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RESULT 4
US-08-431-184-14
; Sequence 14, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,184
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
```

REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-431-184-14

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPAVANGNELLDLSITKVNATEPERT 27
14 FPAVANGNELLDLSITKVNATEPERT 40

RESULT 5
US-08-300-928C-13
Sequence 13, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002,6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-13

Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPAVANGNELLDLSITKVNATEPERT 27
14 FPAVANGNELLDLSITKVNATEPERT 27

Db 14 FPAVANGNELLDLSITKVNATEPERT 40

RESULT 6
US-08-430-944D-13
Sequence 13, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-13

Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FPAVANGNELLDLSITKVNATEPERT 27
14 FPAVANGNELLDLSITKVNATEPERT 40

RESULT 7
US-08-430-014-13
Sequence 13, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA

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/
/      ZIP: 02145
/      COMPUTER READABLE FORM:
/      MEDIUM TYPE: Floppy disk
/      COMPUTER: IBM PC compatible
/      OPERATING SYSTEM: PC-DOS/MS-DOS
/      SOFTWARE: ASCII text
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/08/430,014
/      FILING DATE:
/      CLASSIFICATION:
/      PRIOR APPLICATION DATA:
/      APPLICATION NUMBER: 08/300,928
/      FILING DATE:
/      CLASSIFICATION:
/      ATTORNEY/AGENT INFORMATION:
/      NAME: AMY E. MANDRAGOURAS
/      REGISTRATION NUMBER: 36,207
/      REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (617) 227-7400
/      TELEFAX: (617) 227-5941
/      INFORMATION FOR SEQ ID NO: 13:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 92 amino acids
/      TYPE: amino acid
/      TOPOLOGY: linear
/      MOLECULE TYPE: peptide
/      FRAGMENT TYPE: internal
/      US-08-430-014-13

Query Match      100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSITKVNATEPERT 27
DB      14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 8
US-08-431-184-13
; Sequence 13, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,184
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
```

```
/
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (617)227-7400
/      TELEFAX: (617)742-4214
/      INFORMATION FOR SEQ ID NO: 13:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 92 amino acids
/      TYPE: amino acid
/      TOPOLOGY: linear
/      MOLECULE TYPE: peptide
/      FRAGMENT TYPE: internal
/      US-08-431-184-13

Query Match      100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSITKVNATEPERT 27
DB      14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 9
US-08-300-928C-10
; Sequence 10, Application US/08300928C
; Patent No. 6019772
; GENERAL INFORMATION:
; APPLICANT: GEFTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,928C
; FILING DATE: September 2, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,529
; FILING DATE: December 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
/      US-08-300-928C-10

Query Match      100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSITKVNATEPERT 27
DB      33 FFAVANGNELLDLSITKVNATEPERT 59
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RESULT 10
US-08-430-944D-10
Sequence 10, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-430-944D-10
Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 FFAVANGNELLDLSLTKNATEPERT 27
33 FFAVANGNELLDLSLTKNATEPERT 59
RESULT 11
US-08-430-014-10
Sequence 10, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GERTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
TELEFAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-430-014-10
Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 FFAVANGNELLDLSLTKNATEPERT 27
33 FFAVANGNELLDLSLTKNATEPERT 59
RESULT 12
US-08-431-184-10
Sequence 10, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-431-184-10

Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
|||||
Db 33 FFAVANGNELLDLSLTKNATEPERT 59

RESULT 13
US-07-662-193-5
Sequence 5, Application US/07662193

PATENT No. 5328991
GENERAL INFORMATION:
APPLICANT: Kuo, Mei-chang
APPLICANT: Bond, Julian
TITLE OF INVENTION: Improved Preparation of Cat Dander
TITLE OF INVENTION: Allergens for Immunotherapeutic Purposes and Uses Thereof
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/662,193
FILING DATE: 19910228
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: P36,207
REFERENCE/DOCKET NUMBER: IML89-02AA/IPC-002CC/IMI-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-07-662-193-5

Query Match 100.0%; Score 27; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
|||||
Db 33 FFAVANGNELLDLSLTKNATEPERT 59

RESULT 14
US-07-807-529A-6
Sequence 6, Application US/07807529A

PATENT No. 5547669
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garmen, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBOTOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991

APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/4mi-015

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-807-529A-6

Query Match 100.0%; Score 27; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
|||||
Db 31 FFAVANGNELLDLSLTKNATEPERT 57

RESULT 15
US-08-300-928C-8

Sequence 8, Application US/08300928C
PATENT No. 6019972
GENERAL INFORMATION:

APPLICANT: GEFFER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk


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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/300,928C
: FILING DATE: September 2, 1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/807,529
: FILING DATE: December 13, 1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: AMY E. MANDRAGOURAS
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 109 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-300-928C-8

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Query Match      100.0%; Score 27; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FFAVANGNELLDLSTKVNATPEPT 27
Db      33 FFAVANGNELLDLSTKVNATPEPT 59

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Search completed: October 18, 2005, 13:48:56
Job time : 43 secs

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